SUBSTITUTE SHEET (RULE 26)

FIGURE 1A

ATGGAAAAACTCCATGGGCATGTGTCTGCCCATCCAGACATCCTCTCCT

TGGAGAACCGGTGCCTGGCTATGCTCCCTGACTTACAGCCCTTGGAGAA

ACTACATCAGCATGTATCTACCCACTCAGATATCCTCTCCTTGAAGAAC

CAGTGCCTAGCCACGCTTCCTGACCTGAAGACCATGGAAAAACCACATG

GATATGTGTCTGCCCACCCAGACATCCTCTCCTTGGAGAACCAGTGCCT

GGCCACACTTTCTGACCTGAAGACCATGGAGAAACCACATGGACATGTT

TCTGCCCACCCAGACATCCTCTCCTTGGAGAACCGGTGCCTGGCCACCC

TCCCTAGTCTAAAGAGCACTGTGTCTGCCAGCCCCTTGTTCCAGAGTCT

ACAGATATCTCACATGACGCAAGCTGATTTGTACCGTGTGAACAACAGC

AATTGCCTGCTCTCTGAGCCTCCAAGTTGGAGGGCTCAGCATTTCTCTA

AGGGACTAGACCTTTCAACCTGCCCTATAGCCCTGAAATCCATCTCTGC

CACAGAGACAGCTCAGGAAGCAACTTTGGGTCGTTGGTTTGATTCAGAA

GAGAAGAAAGGGGCAGAGACCCAAATGCCTTCTTATAGTCTGAGCTTGG

GAGAGGAGGAGGAGGTGGAGGATCTGGCCGTGAAGCTCACCTCTGGAGA

CTCTGAATCTCATCCAGAGCCTACTGACCATGTCCTTCAGGAAAAGAAG

ATGGCTCTACTGAGCTTGCTGTGCTCTACTCTGGTCTCAGAAGTAAACA

TGAACAATACATCTGACCCCACCCTGGCTGCCATTTTTGAAATCTGTCG

TGAACTTGCCCTCCTGGAGCCTGAGTTTATCCTCAAGGCATCTTTGTAT

GCCAGGCAGCAGCTGAACGTCCGGAATGTGGCCAATAACATCTTGGCCA

FIGURE 1B

TTGCTGCTTTCTTGCCGGCGTGTCGCCCCCACCTGCGACGATATTTCTG

TGCCATTGTCCAGCTGCCTTCTGACTGGATCCAGGTGGCTGAGCTTTAC

CAGAGCCTGGCTGAGGGAGATAAGAATAAGCTGGTGCCCCTGCCCGCCT

GTCTCCGTACTGCCATGACGGACAAATTTGCCCAGTTTGACGAGTACCA

GCTGGCTAAGTACAACCCTCGGAAGCACCGGGCCAAGAGACACCCCCGC

CGGCCACCCCGCTCTCCAGGGATGGAGCCTCCATTTTCTCACAGATGTT

TTCCAAGGTACATAGGGTTTCTCAGAGAAGAGCAGAGAAAGTTTGAGAA

GGCCGGTGATACAGTGTCAGAGAAAAAGAATCCTCCAAGGTTCACCCTG

AAGAAGCTGGTTCAGCGACTGCACATCCACAAGCCTGCCCAGCACGTTC

AAGCCCTGCTGGGTTACAGATACCCCTCCAACCTACAGCTCTTTTCTCG

AAGTCGCCTTCCTGGGCCTTGGGATTCTAGCAGAGCTGGGAAGAGGATG

AAGCTGTCTAGGCCAGAGACCTGGGAGCGGGAGCTGAGCCTACGGGGGA

ACAAAGCGTCGGTCTGGGAGGAACTCATTGAAAATGGGAAGCTTCCCTT

CATGGCCATGCTTCGGAACCTGTGCAACCTGCTGCGGGTTGGAATCAGT

TCCCGCCACCATGAGCTCATTCTCCAGAGACTCCAGCATGGGAAGTCGG

TGATCCACAGTCGGCAGTTTCCATTCAGATTTCTTAACGCCCATGATGC

CATTGATGCCCTCGAGGCTCAACTCAGAAATCAAGCATTGCCCTTTCCT

TCGAATATAACACTGATGAGGCGGATACTAACTAGAAATGAAAAGAACC

GTCCCAGGCGGAGGTTTCTTTGCCACCTAAGCCGTCAGCAGCTTCGTAT

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WO 00/55315 PCT/US00/06850

FIGURE 1C

GGCAATGAGGATACCTGTGTTGTATGAGCAGCTCAAGAGGGAGAAGCTG

AGAGTACACAAGGCCAGACAGTGGAAATATGATGGTGAGATGCTGAACA

GGTACCGACAGGCCCTAGAGACAGCTGTGAACCTCTCTGTGAAGCACAG

CCTGCCCCTGCTGCCAGGCCGCACTGTCTTGGTCTATCTGACAGATGCT

AATGCAGACAGGCTCTGTCCAAAGAGCAACCCACAAGGGCCCCCGCTGA

ACTATGCACTGCTGTTGATTGGGATGATGATCACGAGGGCGGAGCAGGT

GGACGTCGTGCTGTGTGGAGGTGACACTCTGAAGACTGCAGTGCTTAAG

GCAGAAGAAGGCATCCTGAAGACTGCCATCAAGCTCCAGGCTCAAGTCC

AGGAGTTTGATGAAAATGATGGATGGTCCCTGAATACTTTTGGGAAATA

CCTGCTGTCTCTGGCTGGCCAAAGGGTTCCTGTGGACAGGGTCATCCTC

CTTGGCCAAAGCATGGATGATGGAATGATAAATGTGGCCAAACAGCTTT

ACTGGCAGCGTGTGAATTCCAAGTGCCTCTTTGTTGGTATCCTCCTAAG

AAGGGTACAATACCTGTCAACAGATTTGAATCCCAATGATGTGACACTC

TCAGGCTGTACTGATGCGATACTGAAGTTCATTGCAGAGCATGGGGCCT

CCCATCTTCTGGAACATGTGGGCCAAATGGACAAAATATTCAAGATTCC

ACCACCCCCAGGAAAGACAGGGGTCCAGTCTCTCCGGCCACTGGAAGAG

GACACTCCAAGCCCCTTGGCTCCTGTTTCCCAGCAAGGATGGCGCAGCA

TCCGGCTTTTCATTTCATCCACTTTCCGAGACATGCACGGGGAGCGGGA

CCTGCTGCTGAGGTCTGTGCTGCCAGCACTGCAGGCCCGAGCGGCCCCT

FIGURE 1D

CACCGTATCAGCCTTCACGGAATCGACCTCCGCTGGGGCGTCACTGAGG

AGGAGACCCGTAGGAACAGACAACTGGAAGTGTGCCTTGGGGAGGTGGA

GAACGCACAGCTGTTTGTGGGGATTCTGGGCTCCCGTTATGGATACATT

CCCCCCAGCTACAACCTTCCTGACCATCCACACTTCCACTGGGCCCAGC

AGTACCCTTCAGGGCGCTCTGTGACAGAGATGGAGGTGATGCAGTTCCT

GAACCGGAACCAACGTCTGCAGCCCTCTGCCCAAGCTCTCATCTACTTC

CGGGATTCCAGCTTCCTCAGCTCTGTGCCAGATGCCTGGAAATCTGACT

TTGTTTCTGAGTCTGAAGAGGCCGCATGTCGGATCTCAGAACTGAAGAG

CTACCTAAGCAGACAGAAAGGGATAACCTGCCGCAGATACCCCTGTGAG

TGGGGGGGTGTGGCAGCTGGCCGGCCCTATGTTGGCGGGCTGGAGGAGT

TTGGGCAGTTGGTTCTGCAGGATGTATGGAATATGATCCAGAAGCTCTA

CCTGCAGCCTGGGGCCCTGCTGGAGCAGCCAGTGTCCATCCCAGACGAT

GACTTGGTCCAGGCCACCTTCCAGCAGCTGCAGAAGCCACCGAGTCCTG

CCCGGCCACGCCTTCTTCAGGACACAGTGCAACAGCTGATGCTGCCCCA

CGGAAGGCTGAGCCTGGTGACGGGGCAGTCAGGACAGGGCAAGACAGCC

TTCCTGGCATCTCTTGTGTCAGCCCTGCAGGCTCCTGATGGGGCCAAGG

TGGCACCATTAGTCTTCTTCCACTTTTCTGGGGCTCGTCCTGACCAGGG

TCTTGCCCTCACTCTGCTCAGACGCCTCTGTACCTATCTGCGTGGCCAA

CTAAAAGAGCCAGGTGCCCTCCCCAGCACCTACCGAAGCCTGGTGTGGG

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FIGURE 1E

AGCTGCAGCAGAGGCTGCTGCCCAAGTCTGCTGAGTCCCTGCATCCTGG

CCAGACCCAGGTCCTGATCATCGATGGGGCTGATAGGTTAGTGGACCAG

AATGGGCAGCTGATTTCAGACTGGATCCCAAAGAAGCTTCCCCGGTGTG

TACACCTGGTGCTGAGTGTGTCTAGTGATGCAGGCCTAGGGGAGACCCT

TGAGCAGAGCCAGGGTGCCCACGTGCTGGCCTTGGGGCCTCTGGAGGCC

TCTGCTCGGGCCCGGCTGGTGAGAGAGGAGCTGGCCCTGTACGGGAAGC

GGCTGGAGGAGTCACCATTTAACAACCAGATGCGACTGCTGCTGGTGAA

GCGGGAATCAGGCCGGCCGCTCTACCTGCGCTTGGTCACCGATCACCTG

AGGCTCTTCACGCTGTATGAGCAGGTGTCTGAGAGACTCCGGACCCTGC

CTGCCACTGTCCCCCTGCTGCTGCAGCACATCCTGAGCACACTGGAGAA

GGAGCACGGGCCTGATGTCCTTCCCCAGGCCTTGACTGCCCTAGAAGTC

ACACGGAGTGGTTTGACTGTGGACCAGCTGCACGGAGTGCTGAGTGTGT

GGCGGACACTACCGAAGGGGACTAAGAGCTGGGAAGAAGCAGTGGCTGC

TGGTAACAGTGGAGACCCCTACCCCATGGGCCCGTTTGCCTGCCTCGTC

CAGAGTCTGCGCAGTTTGCTAGGGGAGGGCCCTCTGGAGCGCCCTGGTG

CCCGGCTGTGCCTCCCTGATGGGCCCCTGAGAACAGCAGCTAAACGTTG

CTATGGGAAGAGGCCAGGGCTAGAGGACACGGCACACATCCTCATTGCA

GCTCAGCTCTGGAAGACATGTGACGCTGATGCCTCAGGCACCTTCCGAA

GTTGCCCTCCTGAGGCTCTGGGAGACCTGCCTTACCACCTGCTCCAGAG

Sequence 1 of 5 - 1656 bp

FIGURE 1F

CGGGAACCGTGGACTTCTTTCGAAGTTCCTTACCAACCTCCATGTGGTG

GCTGCACACTTGGAATTGGGTCTGGTCTCTCGGCTCTTGGAGGCCCATG

CCCTCTATGCTTCTTCAGTCCCCAAAGAGGAACAAAAGCTCCCCGAGGC

TGACGTTGCAGTGTTTCGCACCTTCCTGAGGCAGCAGGCTTCAATCCTC

AGCCAGTACCCCCGGCTCCTGCCCCAGCAGGCAGCCAACCAGCCCCTGG

ACTCACCTCTTTGCCACCAAGCCTCGCTGCTCTCCCGGAGATGGCACCT

CCAACACACACTACGATGGCTTAATAAACCCCGGACCATGAAAAATCAG

CAAAGCTCCAGCCTGTCTCTGGCAGTTTCCTCATCCCCTACTGCTGTGG

CCTTCTCCACCAATGGGCAAAGAGCAGCTGTGGGCACTGCCAATGGGAC

AGTTTACCTGTTGGACCTGAGAACTTGGCAGGAGGAGAAGTCTGTGGTG

AGTGGCTGTGATGGAATCTCTGCTTGTTTGTTCCTCTCCGATGATACAC

TCTTTCTTACTGCCTTCGACGGGCTCCTGGAGCTCTGGGACCTGCAGCA

TGGTTGTCGGGTGCTGCAGACTAAGGCTCACCAGTACCAAATCACTGGC

TGCTGCCTGAGCCCAGACTGCCGGCTGCTAGCCACCGTGTGCTTGGGAG

GATGCCTAAAGCTGTGGGACACAGTCCGTGGGCAGCTGGCCTTCCAGCA

CACCTACCCCAAGTCCCTGAACTGTGTTGCCTTCCACCCAGAGGGGCAG

GTAATAGCCACAGGCAGCTGGGCTGGCAGCATCAGCTTCTTCCAGGTGG

ATGGGCTCAAAGTCACCAAGGACCTGGGGGCACCCGGAGCCTCTATCCG

TACCTTGGCCTTCAATGTGCCTGGGGGGGTTGTGGCTGTGGGCCGGCTG

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FIGURE 1G

GACAGTATGGTGGAGCTGTGGGCCTGGCGAGAAGGGGCACGGCTGGCTG

CCTTCCCTGCCCACCATGGCTTTGTTGCTGCTGCGCTTTTCCTGCATGC

GGGTTGCCAGTTACTGACGGCTGGAGAGGATGGCAAGGTTCAGGTGTGG

TCAGGGTCTCTGGGTCGGCCCCGTGGGCACCTGGGTTCCCTTTCTCTCT

CTCCTGCCCTCTCTGTGGCACTCAGCCCAGATGGTGATCGGGTGGCTGT

TGGATATCGAGCGGATGGCATTAGGATCTACAAAATCTCTTCAGGTTCC

CAGGGGGCTCAGGGTCAGGCACTGGATGTGGCAGTGTCCGCCCTGGCCT

GGCTAAGCCCCAAGGTATTGGTGAGTGGTGCAGAAGATGGGTCCTTGCA

GGGCTGGGCACTCAAGGAATGCTCCCTTCAGTCCCTCTGGCTCCTGTCC

AGATTCCAGAAGCCTGTGCTAGGACTGGCCACTTCCCAGGAGCTCTTGG

CTTCTGCCTCAGAGGATTTCACAGTGCAGCTGTGGCCAAGGCAGCTGCT

GACGCGGCCACACAAGGCAGAAGACTTTCCCTGTGGCACTGAGCTGCGG

GGACATGAGGGCCCTGTGAGCTGCTGTAGTTTCAGCACTGATGGAGGCA

GCCTGGCCACCGGGGGCCGGGATCGGAGTCTCCTCTGCTGGGACGTGAG

GACACCCAAAACCCCTGTTTTGATCCACTCCTTCCCTGCCTGTCACCGT

GACTGGGTCACTGGCTGTGCCTGGACCAAAGATAACCTACTGATATCCT

GCTCCAGTGATGGCTCTGTGGGGCTCTGGGACCCAGAGTCAGGACAGCG

GCTTGGTCAGTTCCTGGGTCATCAGAGTGCTGTGAGCGCTGTGGCAGCT

GTGGAGGAGCACGTGGTGTCTGTGAGCCGGGATGGGACCTTGAAAGTGT

Sequence Listing

FIGURE 1H

GGGACCATCAAGGCGTGGAGCTGACCAGCATCCCTGCTCACTCAGGACC

CATTAGCCACTGTGCAGCTGCCATGGAGCCCCGTGCAGCTGGACAGCCT

GGGTCAGAGCTTCTGGTGGTAACCGTCGGGCTAGATGGGGCCACACGGT

TATGGCATCCACTCTTGGTGTGCCAAACCCACACCCTCCTGGGACACAG

CGGCCCAGTCCGTGCTGCTGCTGTTTCAGAAACCTCAGGCCTCATGCTG

ACCGCCTCTGAGGATGGTTCTGTACGGCTCTGGCAGGTTCCTAAGGAAG

CAGATGACACATGTATACCAAGGAGTTCTGCAGCCGTCACTGCTGTGGC

TTGGGCACCAGATGGTTCCATGGCAGTATCTGGAAATCAAGCTGGGGAA

CTAATCTTGTGGCAGGAAGCTAAGGCTGTGGCCACAGCACAGGCTCCAG

GCCACATTGGTGCTCTGATCTGGTCCTCGGCACACACCTTTTTTGTCCT

CAGTGCTGATGAGAAAATCAGCGAGTGGCAAGTGAAACTGCGGAAGGGT

TCGGCACCCGGAAATTTGAGTCTTCACCTGAACCGAATTCTACAGGAGG

ACTTAGGGGTGCTGACAAGTCTGGATTGGGCTCCTGATGGTCACTTTCT

CATCTTGGCCAAAGCAGATTTGAAGTTACTTTGCATGAAGCCAGGGGAT

GCTCCATCTGAAATCTGGAGCAGCTATACAGAAAATCCTATGATATTGT

CCACCCACAAGGAGTATGGCATATTTGTCCTGCAGCCCAAGGATCCTGG

AGTTCTTTCTTTCTTGAGGCAAAAGGAATCAGGAGAGTTTGAAGAGAGG

CTGAACTTTGATATAAACTTAGAGAATCCTAGTAGGACCCTAATATCGA

TAACTCAAGCCAAACCTGAATCTGAGTCCTCATTTTTGTGTGCCAGCTC

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FIGURE 1I

TGATGGGATCCTATGGAACCTGGCCAAATGCAGCCCAGAAGGAGAATGG

ACCACAGGTAACATGTGGCAGAAAAAAGCAAACACTCCAGAAACCCAAA

CTCCAGGGACAGACCCATCTACCTGCAGGGAATCTGATGCCAGCATGGA

TAGTGATGCCAGCATGGATAGTGAGCCAACACCACATCTAAAGACACGG

CAGCGTAGAAAGATTCACTCGGGCTCTGTCACAGCCCTCCATGTGCTAC

CTGAGTTGCTGGTGACAGCTTCGAAGGACAGAGATGTTAAGCTATGGGA

GAGACCCAGTATGCAGCTGCTGGGCCTGTTCCGATGCGAAGGGTCAGTG

AGCTGCCTGGAACCTTGGCTGGGCGCTAACTCCACCCTGCAGCTTGCCG

TGGGAGACGTGCAGGGCAATGTGTACTTTCTGAATTGGGAA

Docket No. 5035.1003-000

FIGURE 2A

ATGGAGAAGCTCTGTGGGCATGTGCCTGGCCATTCAGACATCCTCTCCT

TGAAGAACCGGTGCCTGACCATGCTCCCTGACCTCCAGCCCCTGGAGAA

AATACATGGACATAGATCTGTCCACTCAGACATCCTTTCCTTGGAGAAC

CAGTGTCTGACCATGCTCTCTGACCTCCAGCCCACGGAGAGAATAGATG

GGCATATATCTGTCCACCCAGACATCCTCTCCTTGGAGAATCGGTGCCT

GACCATGCTCCCTGACCTCCAGCCTCTGGAGAAGCTATGTGGACATATG

TCTAGTCATCCAGACGTCCTTTCTTTGGAAAACCAATGTCTAGCTACTC

TCCCCACTGTAAAGAGCACTGCATTGACCAGCCCCTTGCTCCAGGGTCT

TCACATATCTCATACGGCACAAGCTGATCTGCATAGCCTGAAAACTAGC

AACTGCCTGCTCCCTGAGCTTCCTACCAAGAAGACTCCATGTTTCTCTG

AGGAACTAGACCTTCCACCTGGACCCAGGGCCCTGAAATCCATGTCTGC

TACAGCTCAAGTCCAGGAAGTAGCCTTGGGTCAATGGTGTGTCTCCAAA

GAAAAGGAATTTCAAGAAGAAGAAAGCACAGAAGTCCCRATGCCTTTGT

ACAGTCTAAGCTTGGAAGAAGAAGAAGTGGAGGCACCGGTCTTAAAACT

CACATCTGGAGACTCTGGCTTTCATCCTGAAACCACTGACCAGGTCCTT

CAGGAGAAGAAGATGGCTCTCTTGACCTTACTCTGCTCTGCTCTGGCCT

CAAATGTGAATGTGAAAGATGCATCTGACCTTACCCGGGCATCCATCCT

TGAAGTCTGTAGTGCCCTGGCCTCCTTGGAACCGGAGTTCATCCTTAAG

GCATCTTTGTATGCTCGGCAGCAACTTAACCTCCGGGACATCGCCAATA

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FIGURE 2B

CAGTTCTGGCTGTGGCTGCCCTCTTGCCAGCCTGCCGCCCCCATGTACG

ACGGTATTACTCCGCCATTGTTCACCTGCCTTCAGACTGGATCCAGGTA

GCCGAGTTCTACCAGAGCCTGGCAGAAGGGGATGAGAAGAAGTTGGTGT

CCCTGCCTGCCTGTCTCCGAGCTGCCATGACCGACAAATTTGCCGAGTT

TGATGAGTACCAGCTAGCTAAGTACAACCCACGGAAACATCGGTCCAAG

AGGCGGTCCCGCCAGCCACCCCGCCCTCAAAAGACAGAACGTCCATTTT

CAGAGAGAGGGAAATGTTTTCCAAAGAGCCTTTGGCCCCTTAAAAATGA

ACAGATTACGTTTGAAGCAGCTTATAATGCAATGCCAGAGAAAAACAGG

CTACCACGGTTCACTCTGAAGAAGTTGGTAGAGTATCTACATATCCACA

AGCCTGCTCAGCACGTCCAGGCCCTGCTGGGCTACAGGTACCCAGCCAC

CCTAGAGCTCTTTTCTCGGAGTCACCTCCCTGGGCCGTGGGAGTCTAGC

AGAGCTGGTCAGCGGATGAAGCTCCGAAGGCCAGAGACCTGGGAGCGGG

AGCTGAGTTTACGGGGAAACAAAGCTTCTGTGTGGGAGGAGCTCATAGA

CAATGGGAAACTGCCCTTCATGGCCATGCTCCGGAACCTGTGTAACCTG

CTGCGGACTGGGATCAGTGCCCGCCACCATGAACTCGTTCTCCAGAGAC

TCCAGCATGAGAAATCTGTGGTTCACAGTCGGCAGTTTCCATTCAGATT

CCTTAATGCTCATGACTCTATCGATAAACTTGAGGCTCAGCTCAGAAGC

AAAGCATCACCCTTCCCTTCCAATACAACATTGATGAAACGGATAATGA

TTAGAAACTCAAAAAAAAATAGGAGGCCTGCCAGTCGGAAGCACCTGTG

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FIGURE 2C

CACCCTGACGCGCCGGCAGCTTCGGGCAGCAATGACTATACCTGTGATG

TATGAGCAGCTCAAGCGGGAGAAACTGAGGCTGCACAAGGCCAGACAAT

GGAACTGTGATGTTGAGTTGCTGGAGCGCTATCGCCAGGCCCTGGAAAC

AGCTGTGAACCTCTCAGTAAAGCACAACCTATCCCCGATGCCTGGCCGA

ACCCTCTTGGTCTATCTCACAGATGCAAATGCCGACAGGCTCTGTCCCA

AGAGTCACTCACAAGGGCCTCCCCTGAACTATGTGCTGCTGCTGATCGG

AATGATGGTGGCTCGAGCCGAGCAAGTGACTGTTTGCTTGTGTGGGGGA

GGATTTGTGAAGACACCGGTACTTACAGCCGATGAAGGCATCCTGAAGA

CTGCCATCAAACTTCAGGCTCAAGTCCAGGAGTTAGAAGGCAATGATGA

GTGGCCCCTGGACACTTTTGGGAAGTATCTGCTGTCTCTGGCTGTCCAA

AGGACCCCCATTGACAGGGTCATCCTGTTTGGTCAAAGGATGGATACCG

AGCTCCTGAAAGTAGCCAAACAGATTATCTGGCAGCATGTGAATTCCAA

GTGCCTCTTTGTTGGTGTCCTCCTACAGAAAACACAGTACATATCACCA

AATTTGAATCCCAACGATGTGACGCTCTCAGGCTGCACTGACGGGATCC

TGAAATTCATTGCCGAACATGGAGCCTCTCGTCTCCTGGAACATGTGGG

ACAACTAGATAAACTATTCAAGATCCCCCCACCCCCAGGAAAGACACAG

GCACCGTCTCTCCGGCCGCTGGAGGAGAACATCCCTGGTCCCTTGGGTC

CTATTTCCCAGCATGGATGGCGCAATATCCGGCTTTTCATTTCATCCAC

TTTCCGTGACATGCATGGGGAGCGAGATTTGCTGATGAGATCTGTTCTG

FIGURE 2D

CCCGCACTGCAGGCCAGAGTGTTCCCCCACCGCATCAGTCTTCACGCCA

TTGACCTGCGCTGGGGTATCACAGAGGAAGAGACCCGCAGGAACAGACA

ACTGGAAGTGTGCCTTGGGGAGGTGGAGAACTCACAGCTGTTCGTGGGG

ATTCTGGGCTCCCGCTATGGCTACATTCCCCCCAGCTATGATCTTCCTG

ATCATCCCCACTTTCACTGGACCCATGAGTACCCTTCAGGGCGATCCGT

GACAGAGATGGAGGTGATGCAATTCCTGAACCGTGGCCAACGCTCGCAG

CCTTCGGCCCAAGCTCTCATCTACTTCCGAGATCCTGATTTCCTTAGCT

CTGTGCCAGATGCCTGGAAACCTGACTTTATATCTGAGTCAGAAGAAGC

TGCACATCGGGTCTCAGAGCTGAAGAGATATCTACACGAACAGAAAGAG

GTTACCTGTCGCAGCTACTCCTGTGAATGGGGAGGTGTAGCGGCTGGCC

GGCCCTATACTGGGGGCCTGGAGGAGTTTGGACAGTTGGTTCTCCAGGA

TGTGTGGAGCATGATCCAGAAGCAGCACCTGCAGCCTGGGGCCCAGTTG

GAGCAGCCAACATCCATCTCAGAAGACGATTTGATCCAGACCAGCTTTC

AGCAGCTGAAGACCCCAACGAGTCCGGCACGGCCACGCCTTCTTCAGGA

TACAGTGCAGCAGCTGTTGCTGCCCCATGGGAGGCTGAGCCTAGTGACT

GGGCAGGCAGGACAGGGAAAGACTGCCTTTCTGGCATCCCTTGTGTCTG

CCCTGAAGGTCCCTGACCAGCCCAATGAGCCCCCGTTCGTTTTCTTCCA

CTTTGCAGCAGCCCGCCCTGACCAGTGTCTTGCTCTCAACCTCCTCAGA

CGCCTCTGTACCCATCTGCGTCAAAAACTGGGAGAGCTGAGTGCCCTCC

Doc. No. 5-5-1-5-0-0-0-7

FIGURE 2E

CCAGCACTTACAGAGGCCTGGTGTGGGAACTGCAGCAGAAGTTGCTCCT

CAAATTCGCTCAGTCGCTGCAGCCTGCTCAGACTTTGGTCCTTATCATC

GATGGGGCAGATAAGTTGGTGGATCGTAATGGGCAGCTGATTTCAGACT

GGATCCCCAAGTCTCTTCCGCGGCGAGTACACCTGGTGCTGAGTGTGTC

CAGTGACTCAGGCCTGGGTGAGACCCTTCAGCAAAGTCAGGGTGCTTAT

GTGGTGGCCTTGGGCTCTTTGGTCCCATCTTCAAGGGCTCAGCTTGTGA

GAGAAGAGCTAGCACTGTATGGGAAACGACTGGAGGAGTCACCTTTTAA

CAACCAGATGCGGCTGCTGCTGGCAAAGCAGGGTTCAAGCCTGCCATTG

TACCTGCACCTTGTCACTGACTACCTGAGGCTCTTCACACTGTATGAAC

AGGTGTCTGAGAGACTTCGAACCCTGCCCGCCACTCTCCCACTGCTCTT

GCAGCACATCCTGAGCACCTTGGAGCAAGAACATGGCCATGATGTCCTT

CCTCAGGCTTTGACTGCCCTTGAGGTCACACGAAGTGGTCTGACTGTGG

ACCAGCTACATGCAATCCTGAGCACATGGCTGATCTTGCCCAAGGAGAC

TAAGAGCTGGGAAGAAGTGCTGGCTGCCAGTCACAGTGGAAACCCTTTC

CCCTTGTGTCCATTTGCCTACCTTGTCCAGAGTCTACGCAGTTTACTAG

GGGAGGGCCCAGTGGAGCGCCCTGGTGCCCGTCTCTGCCTCTCTGATGG

GCCCCTGAGGACAACAATTAAACGTCGCTATGGGAAAAGGCTGGGGCTA

GAGAAGACTGCGCATGTCCTCATTGCAGCTCACCTCTGGAAGACGTGTG

ATCCTGATGCCTCGGGCACCTTCCGAAGTTGCCCTCCTGAGGCTCTGAA

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FIGURE 2F

AGATTTACCTTACCACCTGCTCCAGAGCGGGAACCATGGTCTCCTTGCC

GAGTTTCTTACCAATCTCCATGTGGTTGCTGCATATCTGGAAGTGGGTC

TAGTCCCCGACCTCTTGGAGGCTCATGTGCTCTATGCTTCTTCAAAGCC

TGAAGCCAACCAGAAGCTCCCAGCGGCAGATGTTGCTGTTTTCCATACC

TTCCTGAGACAACAGGCTTCACTCCTTACCCAGTATCCTTTGCTCCTGC

TCCAGCAGGCAGCTAGCCAGCCTGAAGAGTCACCTGTTTGCTGCCAGGC

CCCCCTGCTCACCCAGCGATGGCACGACCAGTTCACACTGAAATGGATT

AATAAACCCCAGACCCTGAAGGGTCAGCAAAGCTTGTCTCTGACAATGT

CCTCATCCCCAACTGCTGTGGCCTTCTCCCCGAATGGGCAAAGAGCAGC

TGTGGGGACCGCCAGTGGGACAATTTACCTGTTGAACTTGAAAACCTGG

CAGGAGGAGAAGGCTGTGGTGAGTGGCTGTGACGGGATTTCCTCTTTTG

CATTCCTTTCGGACACTGCCCTTTTCCTTACTACCTTCGACGGGCACCT

AGAGCTTTGGGACCTGCAACATGGTTGTTGGGTGTTTCAGACCAAGGCC

CACCAGTACCAAATCACTGGCTGCTGCCTGAGCCCAGACCGCCGCCTGC

TGGCCACTGTGTGTTTGGGAGGATACCTAAAGCTGTGGGACACAGTCCG

AGGACAGCTGGCTTTTCAGTACACCCATCCAAAGTCTCTCAACTGCGTT

GCCTTCCACCCAGAGGGGCAGGTGGTAGCCACAGGCAGCTGGGCTGGCA

GCATTACCTTCTTCCAGGCAGATGGACTCAAAGTCACCAAGGAACTAGG

GGCCCCCGGACCCTCTGTCTGTAGTTTGGCATTCAACAAACCTGGGAAG

Docket No. 95-1-1059

FIGURE 2G

ATTGTGGCTGTGGGCCGGATAGATGGGACAGTGGAGCTGTGGGCCTGGC

AAGAGGGTGCCCGGCTGGCGGCCTTCCCTGCACAGTGTGGCTGTGTCTC

TGCTGTTCTTTTCTTGCATGCTGGAGACCGGTTCCTGACTGCTGGAGAA

GATGGCAAGGCTCAGTTATGGTCAGGATTTCTTGGCCGGCCCAGGGGTT

GCCTGGGCTCTCTTCCTCTTTCTCCTGCACTCTCGGTGGCTCTCAACCC

AGACGGTGACCAGGTGGCTGTTGGGTACCGAGAAGATGGCATTAACATC

TACAAGATTTCTTCAGGTTCCCAGGGGCCTCAGCATCAAGAGCTAAATG

TGGCGGTGTCTGCACTGGTGTGGCTGAGCCCTAGTGTTTTGGTGAGTGG

TGCAGAAGATGGATCCCTGCATGGTTGGATGTTCAAGGGAGACTCCCTT

CATTCCCTGTGGCTGTTGTCGAGATACCAGAAGCCTGTGCTGGGACTGG

CTGCCTCCCGGGAACTCATGGCTGCTGCCTCAGAGGACTTCACTGTGAG

ACTGTGGCCCAGACAGCTGCTGACACAGCCACATGTGCATGCGGTAGAG

TTGCCCTGTTGTGCTGAACTCCGGGGACACGAGGGGCCAGTGTGCTGCT

GTAGCTTCAGCCCTGATGGAGGCATCTTGGCCACAGCTGGCAGGGATCG

GAATCTCCTTTGCTGGGACATGAAGATAGCCCAAGCCCCTCTCCTGATT

CACACTTTCTCGTCCTGTCATCGTGACTGGATCACTGGCTGTGCGTGGA

CCAAAGACAACATCCTGGTCTCCTGCTCGAGTGATGGCTCTGTGGGACT

CTGGAACCCAGAGGCAGGGCAGCAACTTGGCCAGTTCTCAGGCCACCAG

AGTGCCGTGAGCGCCGTGGTTGCTGTGGAGGAACACATTGTATCTGTGA

Sub Spec Filed 6/5/98

FIGURE 2H

GCCGAGATGGGACCTTGAAAGTGTGGGACCATCAGGGTGTGGAGCTGAC

CAGCATCCCTGCCCATTCCGGACCCATCAGCCAGTGTGCAGCTGCTCTG

GAGCCCCGCCCAGGGGGACAGCCTGGATCAGAGCTTCTGGTGGTGACTG

TTGGACTAGATGGGGCCACAAAGTTGTGGCATCCCCTGTTGGTGTGCCA

AATACGTACTCTCCAGGGACACAGTGGCCCAGTCACAGCAGCTGCTGCT

TCAGAGGCCTCAGGCCTCCTGCTGACCTCAGATGATAGCTCTGTACAGC

TCTGGCAGATACCAAAGGAAGCAGATGATTCATACAAACCTAGGAGTTC

TGTGGCCATCACTGCTGTGGCATGGGCACCGGATGGTTCTATGGTGGTG

TCCGGAAATGAAGCCGGGGAACTGACACTGTGGCAGCAAGCCAAGGCTG

TGGCTACCGCACAGGCTCCAGGCCGCGTCAGTCACCTGATCTGGTACTC

GGCAAATTCATTCTTCGTTCTCAGTGCTAATGAAAACGTCAGCGAGTGG

CAAGTGGGACTGAGGAAAGGTTCAACGTCCACCAGTTCCAGTCTTCATC

TGAAGAGAGTTCTGCAGGAGGACTGGGGAGTCTTGACAGGTCTGGGTCT

GGCCCCTGATGGCCAGTCTCTCATCTTGATGAAAGAGGATGTGGAATTA

CTAGAGATGAAGCCTGGGTCTATTCCATCTTCTATCTGCAGGAGGTATG

GAGTACATTCTTCAATACTGTGCACCAGCAAGGAGTACGGCTTGTTCTA

CCTGCAGCAGGGGGACTCCGGATTACTTTCTATATTGGAGCAAAAGGAG

TCAGGGGAGTTTGAAGAGATCCTGGACTTCAATCTGAACTTAAATAATC

CTAATGGGTCCCCAGTATCAATCACTCAGGCCAAACCTGAGTCTGAATC

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FIGURE 2I

ATCCCTTTTGTGCGCCACCTCTGATGGGATGCTGTGGAACTTATCTGAA

TGTACCTCAGAGGGAGAATGGATCGTAGATAACATTTGGCAGAAAAAAG

CAAAAAAACCTAAAACTCAGACTCTGGAGACAGAGTTGTCCCCGCACTC

AGAGTTGGATTTTTCCATTGATTGCTGGATTGATCCCACAAATTTAAAG

GCACAGCAGTGTAAAAAGATCCACTTGGGCTCTGTCACAGCCCTCCATG

TGCTTCCGGGATTGCTGGTGACAGCTTCGAAGGACAGAGATGTTAAGCT

GTGGGAGAGACCCAGTATGCAGCTGCTGGGCTTGTTCCGATGTGAAGGG

CCAGTGAGCTGTCTGGAACCTTGGATGGAGCCCAGCTCTCCCCTGCAGC

TTGCTGTGGGAGACACACAAGGAAACTTGTATTTTCTATCTTGGGAA

Vigene Ex. 2059

FIGURE 3A

MEKLHGHVSAHPDILSLENRCLAMLPDLQPLEKLHQHVSTHSDILSLKN

QCLATLPDLKTMEKPHGYVSAHPDILSLENQCLATLSDLKTMEKPHGHV

SAHPDILSLENRCLATLPSLKSTVSASPLFQSLQISHMTQADLYRVNNS

NCLLSEPPSWRAQHFSKGLDLSTCPIALKSISATETAQEATLGRWFDSE

EKKGAETQMPSYSLSLGEEEEVEDLAVKLTSGDSESHPEPTDHVLQEKK

MALLSLLCSTLVSEVNMNNTSDPTLAAIFEICRELALLEPEFILKASLY

ARQQLNVRNVANNILAIAAFLPACRPHLRRYFCAIVQLPSDWIQVAELY

QSLAEGDKNKLVPLPACLRTAMTDKFAQFDEYQLAKYNPRKHRAKRHPR

RPPRSPGMEPPFSHRCFPRYIGFLREEQRKFEKAGDTVSEKKNPPRFTL

KKLVQRLHIHKPAQHVQALLGYRYPSNLQLFSRSRLPGPWDSSRAGKRM

KLSRPETWERELSLRGNKASVWEELIENGKLPFMAMLRNLCNLLRVGIS

SRHHELILQRLQHGKSVIHSRQFPFRFLNAHDAIDALEAQLRNQALPFP

SNITLMRRILTRNEKNRPRRRFLCHLSRQQLRMAMRIPVLYEQLKREKL

RVHKARQWKYDGEMLNRYRQALETAVNLSVKHSLPLLPGRTVLVYLTDA

NADRLCPKSNPQGPPLNYALLLIGMMITRAEQVDVVLCGGDTLKTAVLK

AEEGILKTAIKLQAQVQEFDENDGWSLNTFGKYLLSLAGQRVPVDRVIL

LGQSMDDGMINVAKQLYWQRVNSKCLFVGILLRRVQYLSTDLNPNDVTL

SGCTDAILKFIAEHGASHLLEHVGQMDKIFKIPPPPGKTGVQSLRPLEE

DTPSPLAPVSQQGWRSIRLFISSTFRDMHGERDLLLRSVLPALQARAAP

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FIGURE 3B

HRISLHGIDLRWGVTEEETRRNRQLEVCLGEVENAQLFVGILGSRYGYI

PPSYNLPDHPHFHWAQQYPSGRSVTEMEVMQFLNRNQRLQPSAQALIYF

RDSSFLSSVPDAWKSDFVSESEEAAXRISELKSYLSRQKGITCRRYPCE

WGGVAAGRPYVGGLEEFGQLVLQDVWNMIQKLYLQPGALLEQPVSIPDD

DLVQATFQQLQKPPSPARPRLLQDTVQXLMLPHGRLSLVTGQSGQGKTA

FLASLVSALQAPDGAKVAXLVFFHFSGARPDQGLALTLLRRLCTYLRGQ

LKEPGALPSTYRSLVWELQQRLLPKSAESLHPGQTQVLIIDGADRLVDQ

NGQLISDWIPKKLPRCVHLVLSVSSDAGLGETLEQSQGAHVLALGPLEA

SARARLVREELALYGKRLEESPFNNQMRLLLVKRESGRPLYLRLVTDHL

RLFTLYEQVSERLRTLPATVPLLLQHILSTLEKEHGPDVLPQALTALEV

TRSGLTVDQLHGVLSVWRTLPKGTKSWEEAVAAGNSGDPYPMGPFACLV

QSLRSLLGEGPLERPGARLCLPDGPLRTAAKRCYGKRPGLEDTAHILIA

AQLWKTCDADASGTFRSCPPEALGDLPYHLLQSGNRGLLSKFLTNLHVV

AAHLELGLVSRLLEAHALYASSVPKEEQKLPEADVAVFRTFLRQQASIL

SQYPRLLPQQAANQPLDSPLCHQASLLSRRWHLQHTLRWLNKPRTMKNQ

QSSSLSLAVSSSPTAVAFSTNGQRAAVGTANGTVYLLDLRTWQEEKSVV

SGCDGISACLFLSDDTLFLTAFDGLLELWDLQHGCRVLQTKAHQYQITG

CCLSPDCRLLATVCLGGCLKLWDTVRGQLAFQHTYPKSLNCVAFHPEGQ

VIATGSWAGSISFFQVDGLKVTKDLGAPGASIRTLAFNVPGGVVAVGRL

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FIGURE 3C

DSMVELWAWREGARLAAFPAHHGFVAAALFLHAGCQLLTAGEDGKVQVW

SGSLGRPRGHLGSLSLSPALSVALSPDGDRVAVGYRADGIRIYKISSGS

QGAQGQALDVAVSALAWLSPKVLVSGAEDGSLQGWALKECSLQSLWLLS

RFQKPVLGLATSQELLASASEDFTVQLWPRQLLTRPHKAEDFPCGTELR

GHEGPVSCCSFSTDGGSLATGGRDRSLLCWDVRTPKTPVLIHSFPACHR

DWVTGCAWTKDNLLISCSSDGSVGLWDPESGQRLGQFLGHQSAVSAVAA

VEEHVVSVSRDGTLKVWDHQGVELTSIPAHSGPISHCAAAMEPRAAGQP

GSELLVVTVGLDGATRLWHPLLVCQTHTLLGHSGPVRAAAVSETSGLML

TASEDGSVRLWQVPKEADDTCIPRSSAAVTAVAWAPDGSMAVSGNQAGE

LILWQEAKAVATAQAPGHIGALIWSSAHTFFVLSADEKISEWQVKLRKG

SAPGNLSLHLNRILQEDLGVLTSLDWAPDGHFLILAKADLKLLCMKPGD

APSEIWSSYTENPMILSTHKEYGIFVLQPKDPGVLSFLRQKESGEFEER

LNFDINLENPSRTLISITQAKPESESSFLCASSDGILWNLAKCSPEGEW

TTGNMWQKKANTPETQTPGTDPSTCRESDASMDSDASMDSEPTPHLKTR

QRRKIHSGSVTALHVLPELLVTASKDRDVKLWERPSMQLLGLFRCEGSV

SCLEPWLGANSTLQLAVGDVQGNVYFLNWE

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FIGURE 4A

MEKLCGHVPGHSDILSLKNRCLTMLPDLQPLEKIHGHRSVHSDILSLEN

QCLTMLSDLQPTERIDGHISVHPDILSLENRCLTMLPDLQPLEKLCGHM

SSHPDVLSLENQCLATLPTVKSTALTSPLLQGLHISHTAQADLHSLKTS

NCLLPELPTKKTPCFSEELDLPPGPRALKSMSATAQVQEVALGQWCVSK

EKEFQEEESTEVPMPLYSLSLEEEEVEAPVLKLTSGDSGFHPETTDQVL

QEKKMALLTLLCSALASNVNVKDASDLTRASILEVCSALASLEPEFILK

ASLYARQQLNLRDIANTVLAVAALLPACRPHVRRYYSAIVHLPSDWIQV

AEFYQSLAEGDEKKLVSLPACLRAAMTDKFAEFDEYQLAKYNPRKHRSK

RRSRQPPRPQKTERPFSERGKCFPKSLWPLKNEQITFEAAYNAMPEKNR

LPRFTLKKLVEYLHIHKPAQHVQALLGYRYPATLELFSRSHLPGPWESS

RAGQRMKLRRPETWERELSLRGNKASVWEELIDNGKLPFMAMLRNLCNL

LRTGISARHHELVLQRLQHEKSVVHSRQFPFRFLNAHDSIDKLEAQLRS

KASPFPSNTTLMKRIMIRNSKKNRRPASRKHLCTLTRRQLRAAMTIPVM

YEQLKREKLRLHKARQWNCDVELLERYRQALETAVNLSVKHNLSPMPGR

TLLVYLTDANADRLCPKSHSQGPPLNYVLLLIGMMVARAEQVTVCLCGG

GFVKTPVLTADEGILKTAIKLQAQVQELEGNDEWPLDTFGKYLLSLAVQ

RTPIDRVILFGQRMDTELLKVAKQIIWQHVNSKCLFVGVLLQKTQYISP

NLNPNDVTLSGCTDGILKFIAEHGASRLLEHVGQLDKLFKIPPPPGKTQ

APSLRPLEENIPGPLGPISQHGWRNIRLFISSTFRDMHGERDLLMRSVL

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FIGURE 4B

PALQARVFPHRISLHAIDLRWGITEEETRRNRQLEVCLGEVENSQLFVG

ILGSRYGYIPPSYDLPDHPHFHWTHEYPSGRSVTEMEVMQFLNRGQRSQ

PSAQALIYFRDPDFLSSVPDAWKPDFISESEEAAHRVSELKRYLHEQKE

VTCRSYSCEWGGVAAGRPYTGGLEEFGQLVLQDVWSMIQKQHLQPGAQL

EQPTSISEDDLIQTSFQQLKTPTSPARPRLLQDTVQQLLLPHGRLSLVT

GQAGQGKTAFLASLVSALKVPDQPNEPPFVFFHFAAARPDQCLALNLLR

RLCTHLRQKLGELSALPSTYRGLVWELQQKLLLKFAQSLQPAQTLVLII

DGADKLVDRNGQLISDWIPKSLPRRVHLVLSVSSDSGLGETLQQSQGAY

VVALGSLVPSSRAQLVREELALYGKRLEESPFNNQMRLLLAKQGSSLPL

YLHLVTDYLRLFTLYEQVSERLRTLPATLPLLLQHILSTLEQEHGHDVL

PQALTALEVTRSGLTVDQLHAILSTWLILPKETKSWEEVLAASHSGNPF

PLCPFAYLVQSLRSLLGEGPVERPGARLCLSDGPLRTTIKRRYGKRLGL

EKTAHVLIAAHLWKTCDPDASGTFRSCPPEALKDLPYHLLQSGNHGLLA

EFLTNLHVVAAYLEVGLVPDLLEAHVLYASSKPEANQKLPAADVAVFHT

FLRQQASLLTQYPLLLLQQAASQPEESPVCCQAPLLTQRWHDQFTLKWI

NKPQTLKGQQSLSLTMSSSPTAVAFSPNGQRAAVGTASGTIYLLNLKTW

QEEKAVVSGCDGISSFAFLSDTALFLTTFDGHLELWDLQHGCWVFQTKA

HQYQITGCCLSPDRRLLATVCLGGYLKLWDTVRGQLAFQYTHPKSLNCV

AFHPEGQVVATGSWAGSITFFQADGLKVTKELGAPGPSVCSLAFNKPGK

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FIGURE 4C

IVAVGRIDGTVELWAWQEGARLAAFPAQCGCVSAVLFLHAGDRFLTAGE

DGKAQLWSGFLGRPRGCLGSLPLSPALSVALNPDGDQVAVGYREDGINI

YKISSGSQGPQHQELNVAVSALVWLSPSVLVSGAEDGSLHGWMFKGDSL

HSLWLLSRYQKPVLGLAASRELMAAASEDFTVRLWPRQLLTQPHVHAVE

LPCCAELRGHEGPVCCCSFSPDGGILATAGRDRNLLCWDMKIAQAPLLI

HTFSSCHRDWITGCAWTKDNILVSCSSDGSVGLWNPEAGQQLGQFSGHQ

SAVSAVVAVEEHIVSVSRDGTLKVWDHQGVELTSIPAHSGPISQCAAAL

EPRPGGQPGSELLVVTVGLDGATKLWHPLLVCQIRTLQGHSGPVTAAAA

SEASGLLLTSDDSSVQLWQIPKEADDSYKPRSSVAITAVAWAPDGSMVV

SGNEAGELTLWQQAKAVATAQAPGRVSHLIWYSANSFFVLSANENVSEW

QVGLRKGSTSTSSSLHLKRVLQEDWGVLTGLGLAPDGQSLILMKEDVEL

LEMKPGSIPSSICRRYGVHSSILCTSKEYGLFYLQQGDSGLLSILEQKE

SGEFEEILDFNLNLNNPNGSPVSITQAKPESESSLLCATSDGMLWNLSE

CTSEGEWIVDNIWQKKAKKPKTQTLETELSPHSELDFSIDCWIDPTNLK

AQQCKKIHLGSVTALHVLPGLLVTASKDRDVKLWERPSMQLLGLFRCEG

PVSCLEPWMEPSSPLQLAVGDTQGNLYFLSWE

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FIGURE 5A

CACGCGTCCGGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGG

CCCCGGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCG

CTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTC

GTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACC

CGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTG

GGACGCACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGC

CTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCG

CGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGG

GGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTACCTGCCCAAC

ACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGC

GCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCT

CTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCG

CTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTA

GTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGT

CAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGG

CGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGC

GTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTG

GGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTG

GTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGC

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FIGURE 5B

TCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGC

GGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGT

CCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACA

AGGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCT

GACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCC

TGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACT

GGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTG

CCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTC

ACCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGG

CGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCT

CCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGC

CTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAAC

GCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGC

CAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGC

GCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGC

ACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCTGATGAG

TGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACC

ACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCA

AGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCG

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FIGURE 5C

GGAGCTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCC

CTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGC

CGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGA

AAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTG

CTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGC

TGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGT

GCGGGCCCAGGACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTG

ACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCG

CCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGT

GGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTC

ACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAG

CTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGC

TTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGT

GCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCT

GTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACC

TCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA

GTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTA

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FIGURE 5D

GAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACG

GCCTAT

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FIGURE 6A

HASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATF

VRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSC

LKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPN

TVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPP

LYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARR

RGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCV

VSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPC

PPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRP

WMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAV

TPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRAC

LRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDC

AWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET

TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPA

LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSV

LNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDV

TGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSH

VSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLR

FMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRD

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FIGURE 6B

GLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPV

EDEALGGTAFVQMPAHGL

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FIGURE 7

TCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACT

ACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT

TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGT

GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCA

ACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGC

AGCTCCCATTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCA

TCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGA

TGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGT

GGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACG

TGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCC

CGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAG

ACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA

GACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGC

CCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCG

AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGT

CCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCT

GGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCA

CTCCCCACATAGGAATAGTCCATCCCCTGAT

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FIGURE 8A

CCACGCGTCCGGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCC

GGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCT

GCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGG

GCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCT

GGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCCGCCGC

CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCA

GAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCT

GGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA

CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCT

GCTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCT

CTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTA

CCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCG

AAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGT

CCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCG

AAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCG

GACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAG

TGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTC

TTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA

GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCC

TTGTCCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAA

FIGURE 8B

GGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGG

CGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG

GACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCT

GTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAA

GACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCG

GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCG

TCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCTT

CGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA

CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCA

TGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGC

TTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCT

GCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGT

CGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAG

GCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAG

ACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCA

GCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAA

GCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAAC

GTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT

CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGT

GCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCG

Attorney Docket: 3575.1050-000

FIGURE 8C

GGCCCAGGACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGC

GTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAA

ACCCCAGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCA

TGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCA

GCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA

TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTT

CGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTC

CTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG

CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGA

CGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCAC

CCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTG

CGTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCT

GGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGG

CCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGC

CCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAG

GAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTT

TCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGAT

CCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA

TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGC

CTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGC

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FIGURE 8D

CAAGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCA

AGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGG

GTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCT

GACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCAT

CCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCC

CTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCC

CGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTC

CGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT

GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCC

ACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGG

AATAGTCCATCCCCTGAT

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FIGURE 9A

HASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATF

VRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSC

LKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPN

TVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPP

LYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARR

RGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCV

VSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPC

PPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRP

WMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAV

TPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRAC

LRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDC

AWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET

TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPA

LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSV

LNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDV

TGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSH

VSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLR

FMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRD

GLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPV

Sequence 5 of 5 of 5

FIGURE 9B

EDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASL

TFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLL

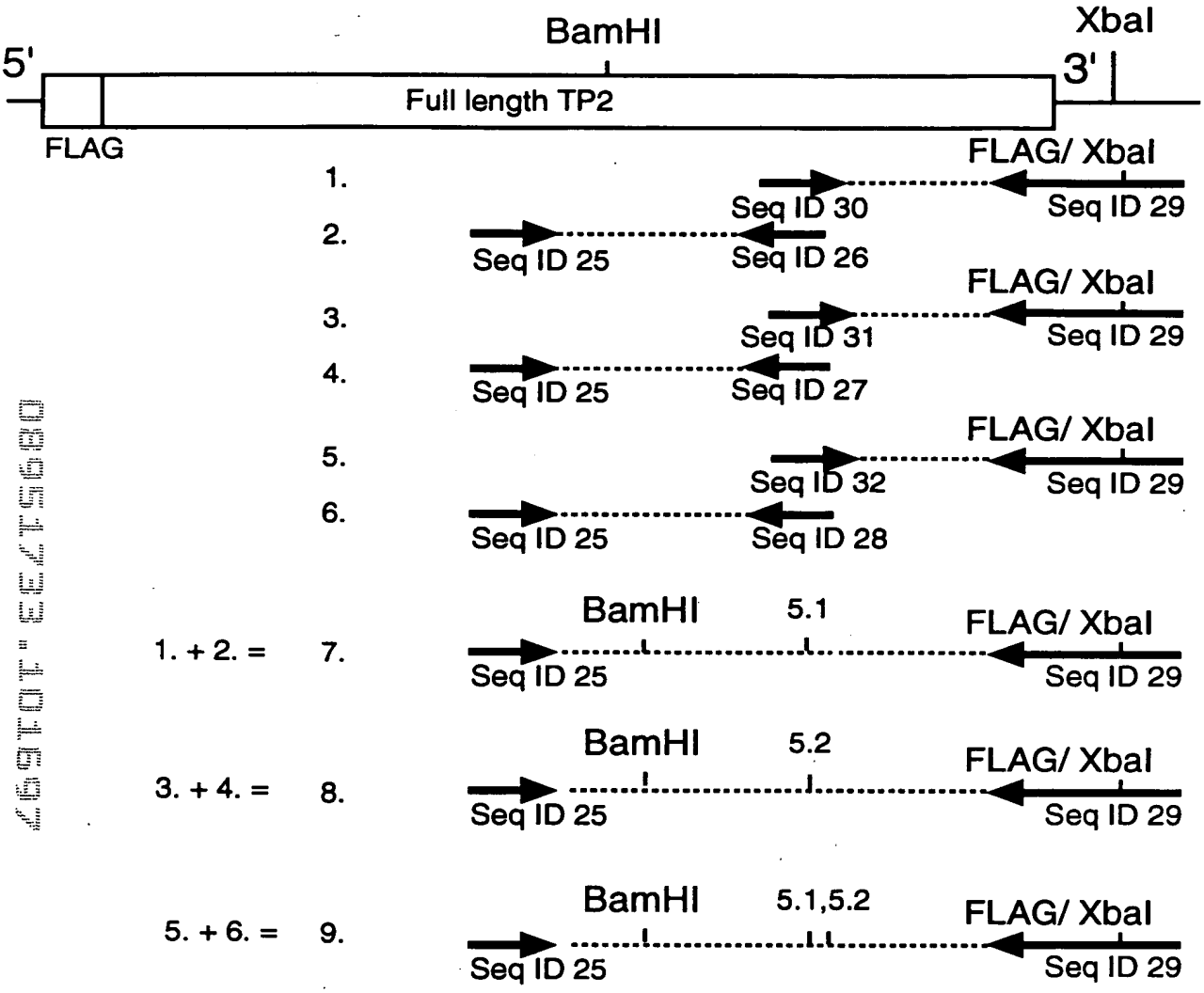
QAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL

GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSR

KLPGTTLTALEAAANPALPSDFKTILD

Sequence: 6 of 6

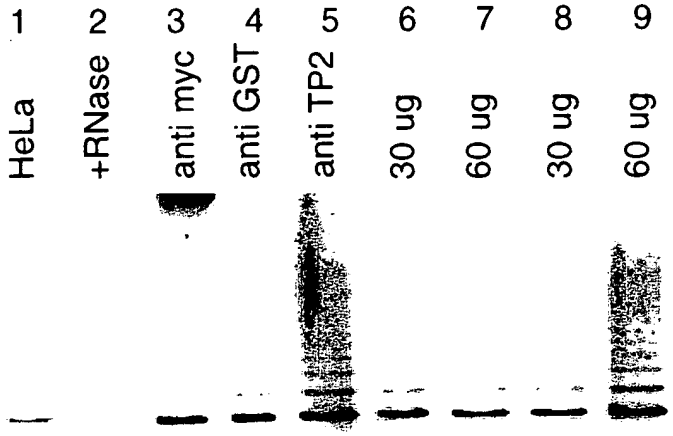
FIG. 10



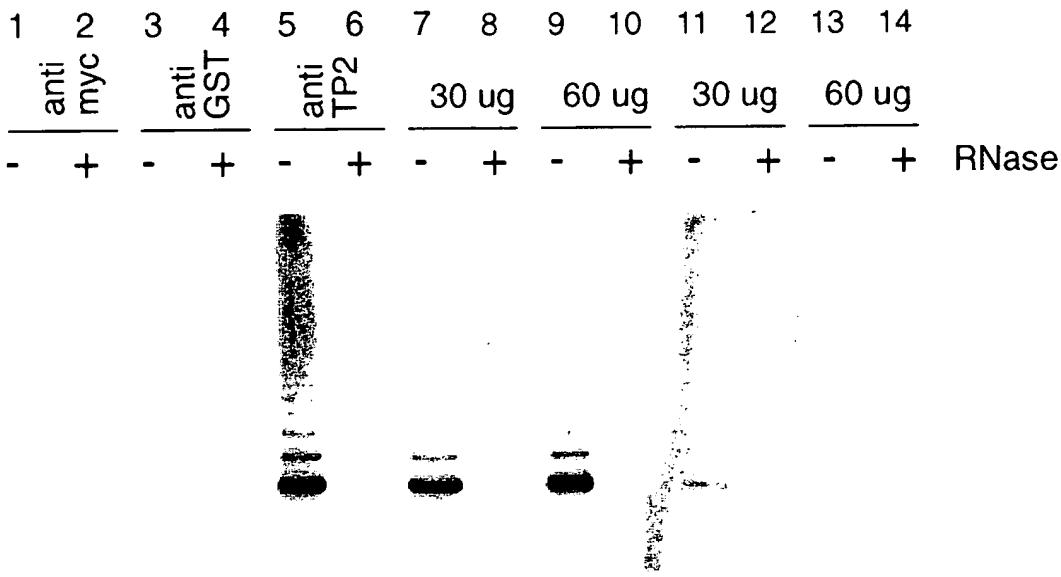
SUBSTITUTE SHEET (RULE 26)

FIG. 11

A


1
2
3
4
5
6
7
8
9
HeLa
+RNase
anti myc
anti GST
anti TP2
30 ug
60 ug
30 ug
60 ug

B


1 2 3 4 5 6 7 8 9 10 11 12 13 14
anti myc
anti GST
anti TP2
30 ug
60 ug
30 ug
60 ug
- + - + - + - + - + - + - + RNase

C

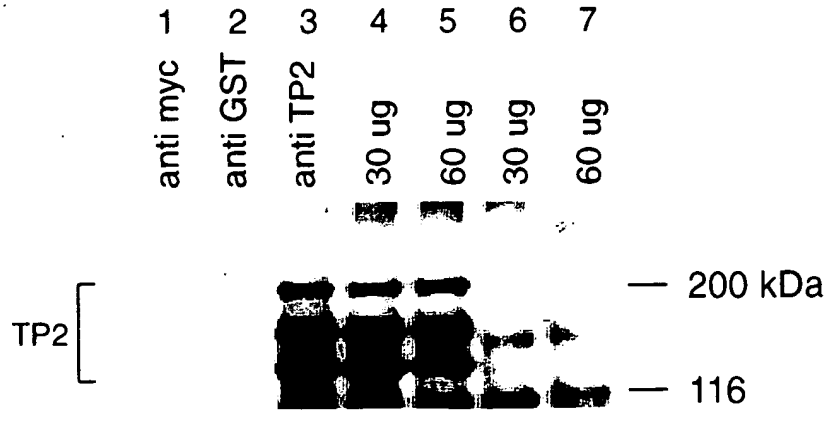
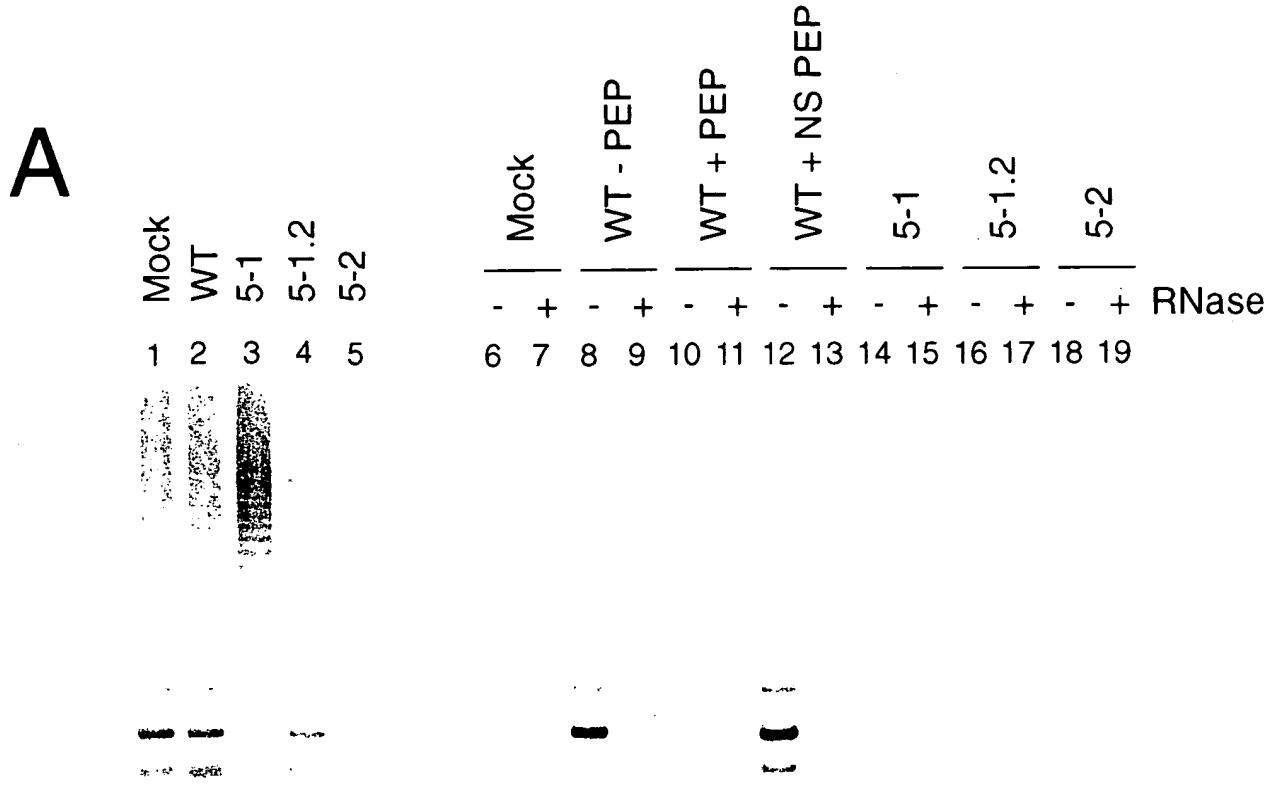

1
2
3
4
5
6
7
anti myc
anti GST
anti TP2
30 ug
60 ug
30 ug
60 ug
TP2
200 kDa
116

FIG. 12


A
Mock
WT
5-1
5-1.2
5-2
Mock
WT - PEP
WT + PEP
WT + NS PEP
5-1
5-1.2
5-2
- + - + - + - + - + - + - + RNase
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

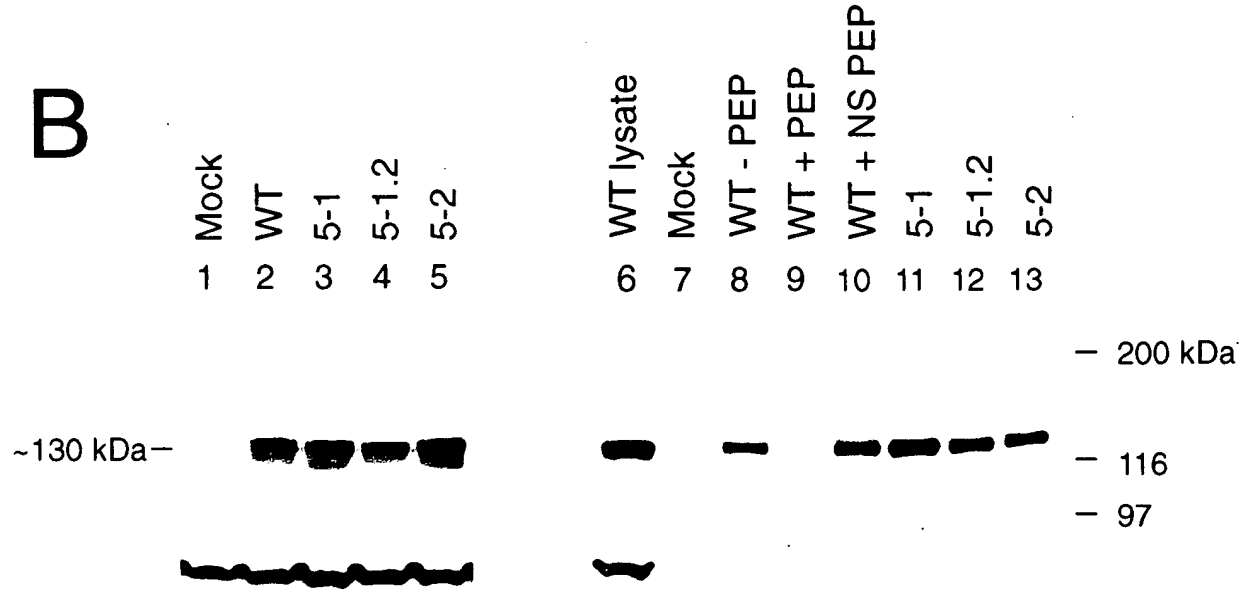
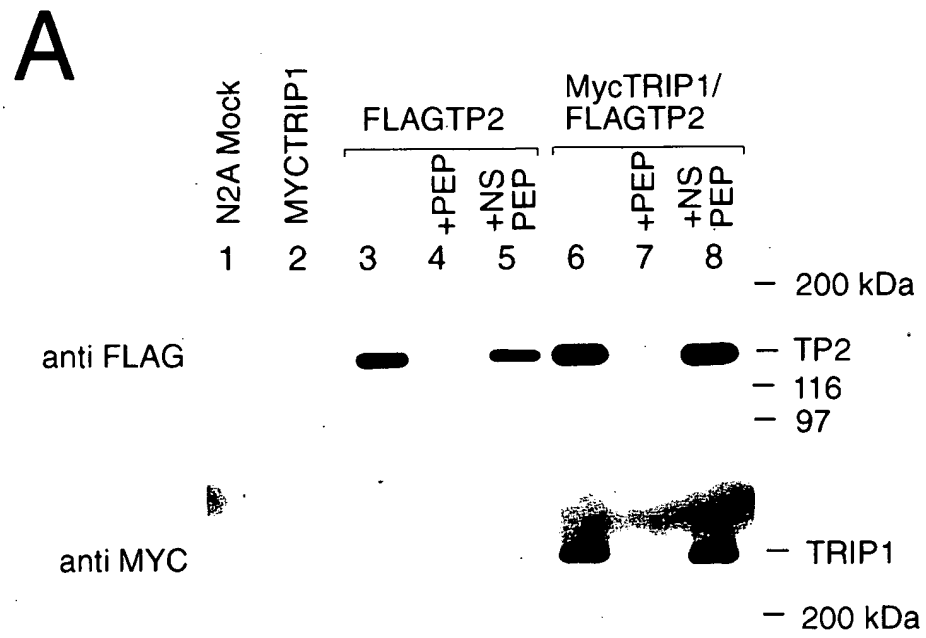

B
Mock
WT
5-1
5-1.2
5-2
WT lysate
Mock
WT - PEP
WT + PEP
WT + NS PEP
5-1
5-1.2
5-2
1 2 3 4 5 6 7 8 9 10 11 12 13
200 kDa
~130 kDa
116
97

FIG. 13


A
N2A Mock
MYCTRIP1
FLAGTP2
+PEP
+NS PEP
MycTRIP1/ FLAGTP2
+PEP
+NS PEP
1 2 3 4 5 6 7 8
200 kDa
anti FLAG
TP2
116
97
anti MYC
TRIP1
200 kDa

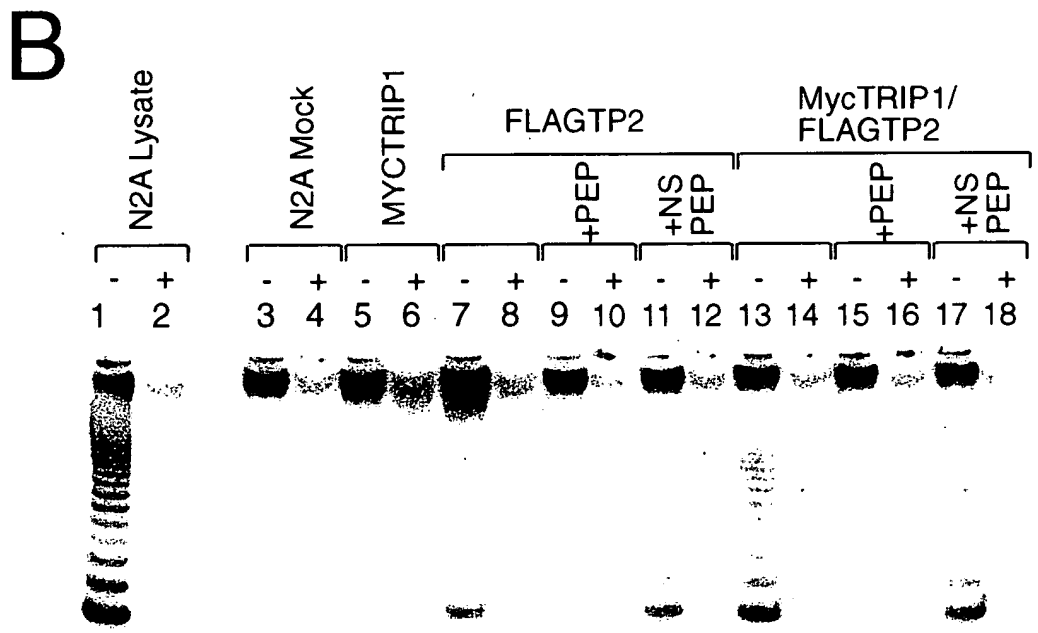
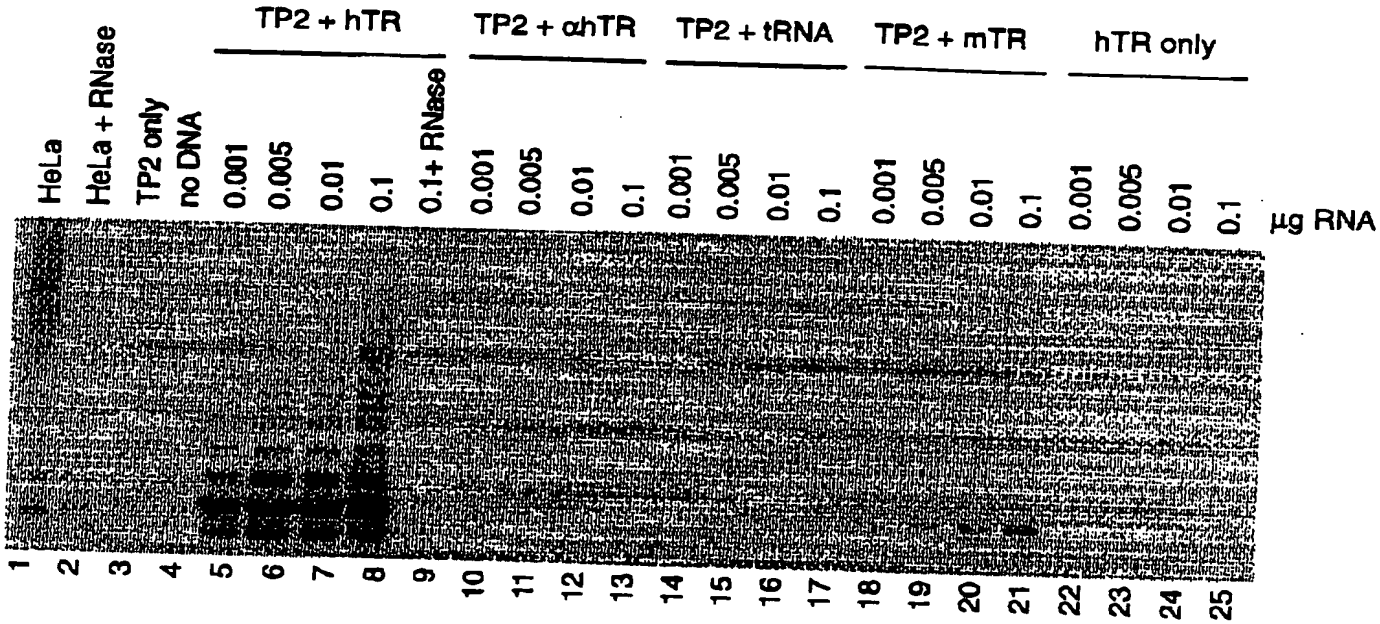
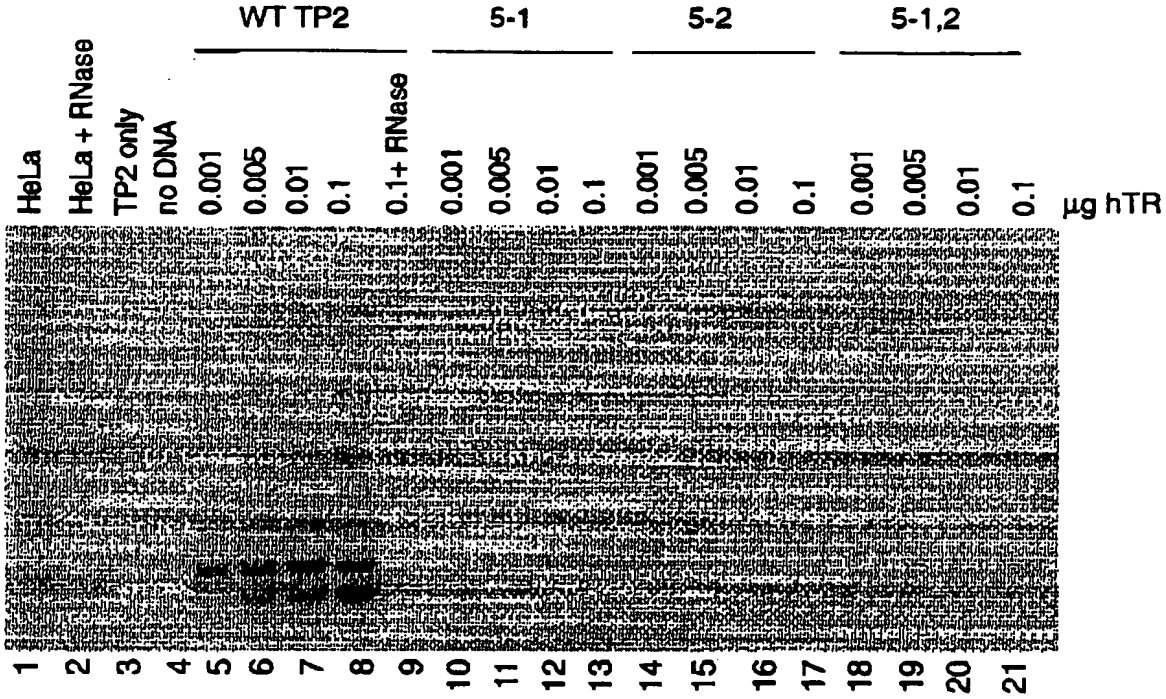

B
N2A Lysate
N2A Mock
MYCTRIP1
FLAGTP2
+PEP
+NS PEP
MycTRIP1/ FLAGTP2
+PEP
+NS PEP
- + - + - + - + - + - + - + - + - +
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

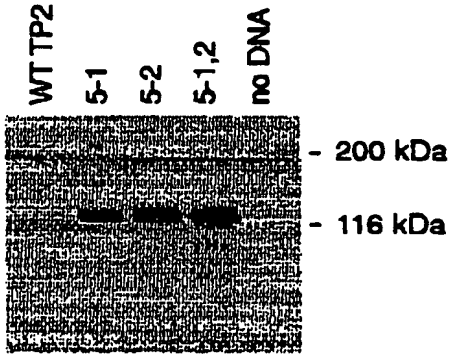
FIG. 14



BEST AVAILABLE COPY

FIG. 15





BEST AVAILABLE COPY

FIG. 16

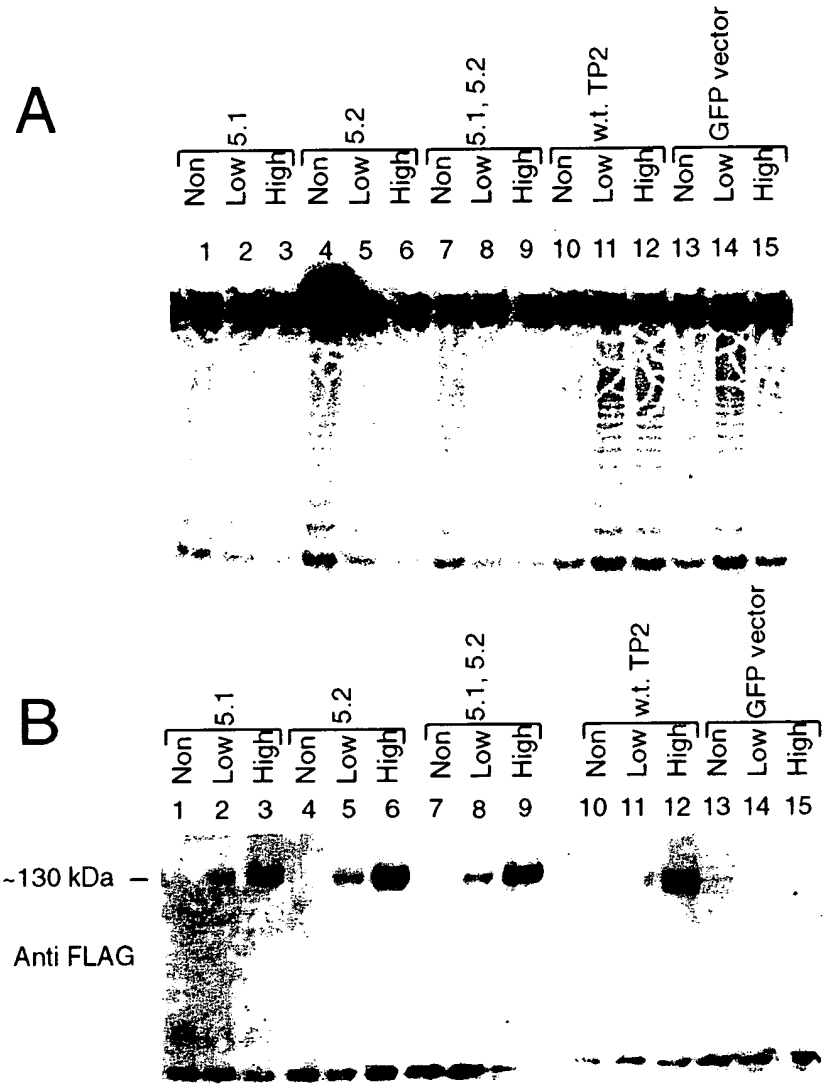

A
Non
Low
High
5.1
5.2
5.1, 5.2
w.t. TP2
GFP vector
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
B
~130 kDa
Anti FLAG

FIG. 17

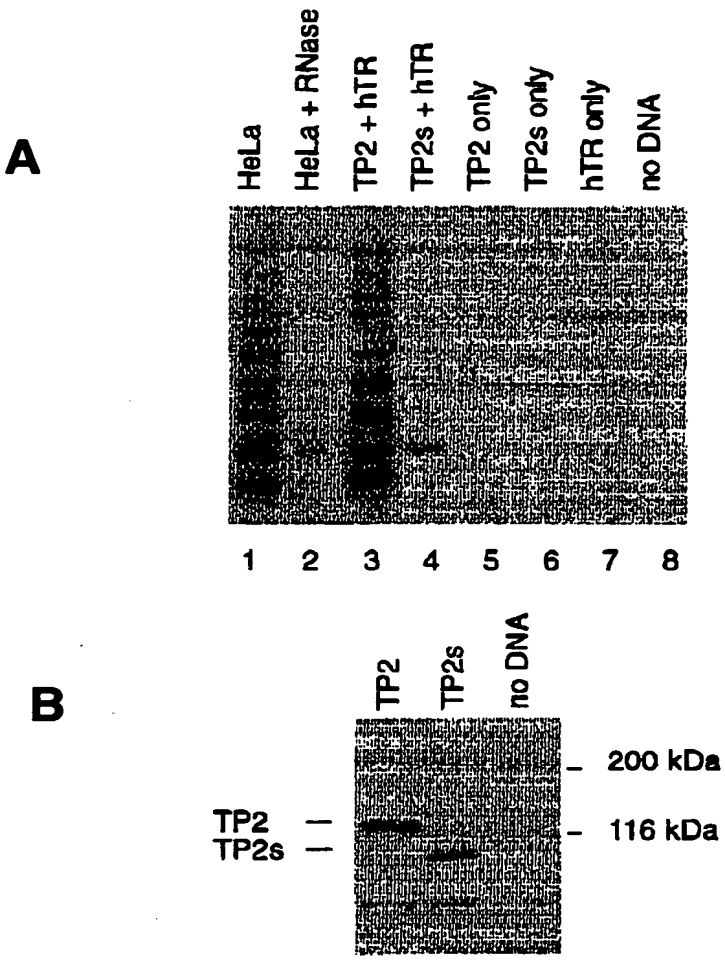
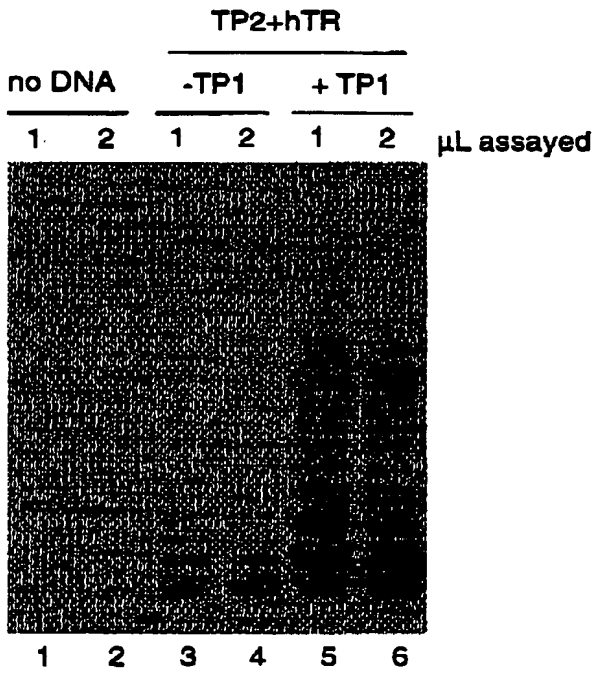

A
HeLa
HeLa + RNase
TP2 + hTR
TP2s + hTR
TP2 only
TP2s only
hTR only
no DNA
1 2 3 4 5 6 7 8
B
TP2
TP2s
no DNA
200 kDa
116 kDa
TP2
TP2s

FIG. 18



BEST AVAILABLE COPY